

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:26:53 : Search time 31.6762 Seconds
(without alignments)
2795.154 Million cell updates/sec

US-10-054-680-2

Sequence: 1 MAMLRLOPLTSAFLHFGVLT.....LWLLYLDFATLEAVCYIKGF 921

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*
1: plr1:*
2: plr2:*
3: plr3:*
4: plr4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|---------------------|
| 1 | 3447.5 | 71.9 | 970 | 2 A36417 | Na+/Ca2+-exchangin |
| 2 | 3441 | 71.7 | 935 | 2 S43730 | Na+/Ca2+-exchangin |
| 3 | 3439.5 | 71.7 | 973 | 2 S32815 | Na+/Ca2+-exchangin |
| 4 | 3437.5 | 71.7 | 941 | 2 B53335 | Na+/Ca2+-exchangin |
| 5 | 3434.5 | 71.6 | 958 | 2 S32435 | Na+/Ca2+-exchangin |
| 6 | 3432.5 | 71.6 | 970 | 2 I48097 | Na+/Ca2+-exchangin |
| 7 | 3426 | 71.4 | 957 | 2 A53789 | Na+/Ca2+-exchangin |
| 8 | 3425.5 | 71.4 | 970 | 2 S27114 | Na+/Ca2+-exchangin |
| 9 | 3422 | 71.3 | 971 | 2 S28833 | Na+/Ca2+-exchangin |
| 10 | 3357 | 70.0 | 921 | 2 A54139 | Na+/Ca2+-exchangin |
| 11 | 2007 | 41.8 | 890 | 2 B89047 | protein C10G8.5 [i |
| 12 | 1192 | 24.8 | 807 | 2 T24110 | hypothetical prote |
| 13 | 659 | 13.7 | 152 | 2 I52640 | cardiac sodium/cal |
| 14 | 573.5 | 12.0 | 538 | 2 T00424 | probable Na+/Ca2+ |
| 15 | 573 | 11.9 | 133 | 2 A48852 | Na+/Ca2+-exchangin |
| 16 | 312 | 6.5 | 1199 | 2 S20969 | Na+/Ca2+, K+-exchan |
| 17 | 284.5 | 5.9 | 1014 | 2 T31433 | Na+/Ca2+, K+-exchan |
| 18 | 225 | 4.7 | 123 | 2 I46959 | Na/Ca exchanger NA |
| 19 | 215.5 | 4.5 | 591 | 2 T19746 | hypothetical prote |
| 20 | 205.5 | 4.3 | 1568 | 2 T08616 | aggregation factor |
| 21 | 201 | 4.2 | 4936 | 2 AH2515 | hypothetical prote |
| 22 | 190.5 | 4.0 | 2205 | 2 T08615 | aggregation factor |
| 23 | 170.5 | 3.6 | 611 | 2 T21747 | hypothetical prote |
| 24 | 169.5 | 3.5 | 3016 | 2 S77300 | hypothetical prote |
| 25 | 161 | 3.4 | 825 | 2 T08617 | aggregation factor |
| 26 | 150.5 | 3.1 | 591 | 2 S40705 | Na+/Ca2+, K+-exchan |
| 27 | 147 | 3.0 | 590 | 2 S40707 | hypothetical prote |
| 28 | 144.5 | 3.0 | 703 | 2 T03888 | Na+/Ca2+, K+-exchan |
| 29 | 144 | 3.0 | 644 | 2 B96582 | hypothetical prote |

| | | | | | |
|----|-------|-----|------|----------|--------------------|
| 30 | 144 | 3.0 | 1428 | 2 AC2224 | hypothetical prote |
| 31 | 143.5 | 3.0 | 325 | 2 F65110 | hypothetical 34.7 |
| 32 | 143 | 3.0 | 123 | 2 A53335 | Na+/Ca2+-exchangin |
| 33 | 142.5 | 3.0 | 325 | 2 C91138 | hypothetical prote |
| 34 | 142.5 | 3.0 | 325 | 2 F85983 | hypothetical prote |
| 35 | 142.5 | 3.0 | 1807 | 2 JC6319 | integrin beta-4 ch |
| 36 | 142 | 3.0 | 302 | 2 C64311 | Na+/Ca2+-exchangin |
| 37 | 141.5 | 2.9 | 318 | 2 G84196 | cation antiporter |
| 38 | 139.5 | 2.9 | 825 | 2 AB1841 | hypothetical prote |
| 39 | 139.5 | 2.9 | 1748 | 1 JN0786 | integrin beta-4 ch |
| 40 | 138 | 2.9 | 743 | 2 T38674 | probable membrane |
| 41 | 135.5 | 2.8 | 325 | 2 A10904 | probable membrane |
| 42 | 134 | 2.8 | 433 | 2 S74922 | hypothetical prote |
| 43 | 132 | 2.8 | 720 | 2 T02457 | hypothetical prote |
| 44 | 129.5 | 2.7 | 309 | 2 B72342 | conserved hypotet |
| 45 | 128.5 | 2.7 | 664 | 2 S66067 | methionine-tRNA 11 |

ALIGNMENTS

| | | | | | | | | | |
|---|-----|---|-----|-------|---------------|-------|-------------|--|--|
| RESULT 1 | | | | | | | | | |
| A36417 Na+/Ca2+-exchanging protein - dog | | | | | | | | | |
| C:Species: Canis lupus familiaris (dog) | | | | | | | | | |
| C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_Change 18-Aug-2000 | | | | | | | | | |
| C:Accession: A36417 | | | | | | | | | |
| R:Nicolli, D.A.; Longoni, S.; Philippson, K.D. | | | | | | | | | |
| Science 250, 562-565, 1990 | | | | | | | | | |
| A:Title: Molecular cloning and functional expression of the cardiac sarcolemmal Na(+) | | | | | | | | | |
| A:Reference number: A36417; MUID:91047958; PMID:1700476 | | | | | | | | | |
| A:Accession: A36417 | | | | | | | | | |
| A>Status: preliminary | | | | | | | | | |
| A:Molecule type: mRNA | | | | | | | | | |
| A:Residues: 1-970 <NIC> | | | | | | | | | |
| A:Cross-references: GB:M57523; NID:G164072; PIDN:AAA62766.1; PID:G164073; GB:M36119 | | | | | | | | | |
| C:Superfamily: human Na+/Ca2+-exchanging protein | | | | | | | | | |
| C:Keywords: phosphoprotein; transmembrane protein | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity 69.2%; Pred. No. 8.4e-224; | | | | | | | | | |
| Matches 677; Conservative 109; Mismatches 127; Indels 65; Gaps 10; | | | | | | | | | |
| QY | 1 | MAMLRLOPLTSAFLHFGVLTFLF--LNGLRNAGSGDVPSTGONNESCSSSPCKRGV | 58 | 71.9% | Score 3447.5; | DB 2; | Length 970; | | |
| DB | 1 | MLQLRLPFSMGCHLVALLFSHVDLISETMBEGNETGE---CTGSIYCKRGV | 56 | | | | | | |
| QY | 59 | ILPIVYPNPISLGDRIARVYFVALIYMFGLGSIADRFMASIVITISOEREVTIKRPN | 118 | | | | | | |
| DB | 57 | ILPIVPEPDPSFGDKIARATYFVAMVYMFGLGSIADRFMASIVITISOEREVTIKRPN | 116 | | | | | | |
| QY | 119 | GETSTPTIRVWNETVSNLTMLAGSSAPDILLILEVCGHGFIAGDLGPSTVGSAAAFNM | 178 | | | | | | |
| DB | 117 | GETSTPTIRVWNETVSNLTMLAGSSAPDILLILEVCGHGFIAGDLGPSTVGSAAAFNM | 176 | | | | | | |
| QY | 179 | FIITICVYVVPDGETRIKIKHVRFFITRAWSIFAYIMLMLAIFSGVGVYMGSLTL | 238 | | | | | | |
| DB | 177 | FIITICVYVVPDGETRIKIKHVRFFITRAWSIFAYIMLMLAIFSGVGVYMGSLTL | 236 | | | | | | |
| QY | 239 | FFPVCVLLAAVADRRLFFYKTMHKKYRTDKRGIIETEGDPKPG---IEMDGKMNSH | 295 | | | | | | |
| DB | 237 | FFPVCVLLAAVADRRLFFYKTMHKKYRTDKRGIIETEGDPKPG---IEMDGKMNSH | 296 | | | | | | |
| QY | 296 | --FLDGNLVPLEGEVD---ESRREMIKLIKDKOKHPEKDLQVLVEMANYALSHQO | 348 | | | | | | |
| DB | 297 | VDFNFDGALV--LEVDRODDDEARREMARILKEKOKHPEKDLQVLVEMANYALSHQO | 355 | | | | | | |
| QY | 349 | KSRATYRIQATPMATGAGNIILKKHAEOAKKASSSVHTDEPE--DFISKVFDPDCSQOC | 407 | | | | | | |
| DB | 356 | KSRATYRIQATPMATGAGNIILKKHAEOAKKASSSVHTDEPE--DFISKVFDPDCSQOC | 415 | | | | | | |
| QY | 408 | LENCAGVLTIVVRKGGDSKTYVDYKTEEDGSANAGADYEFTEGVTVLKPGETQEFESVG | 467 | | | | | | |

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Db 416 LENCSTVALTIIRGGDLNTVTVDFRTEDGTANAGSDYEETEGVYFKRGFTOKETIRNG 475
Qy 468 IIDDIDFEDEHEFVRLSNVRIEEOPEEGMPRAIFNSLPLRAVLASPCVATVITLDDO 527
Db 476 IIDDIDFEDEENLVLHLSNVKVSSEASDEGILANHVS--ALACGSPSTAVTITFDDO 532
Qy 528 HAGIFPEECDTIHVSISIGMEYKVLRTSGARCTVIVPRTVEGTAKGGGEDEDTYGGEL 587
Db 533 HAGIFPEEVEVTHSESIGIMEYKVLRTSGARGNVIVPYKTIEGTARGGGEDEDTYGGEL 592
Qy 588 EKFNDVTYTKIRKIYDEEYERQENFIALGEPKMERG----- 627
Db 593 EFNNDIVTKISVYKVIDDEEYERQENFIALGEPKMERG----- 652
Qy 628 -----ISDYTDK--LTMEEEKARIAEMGKPYLGEPKLEVI 663
Db 653 YGQPVKRYKHAREHPIRSTVYITIAEYDOKPRLTSKEEERRIAEKGRPLTSGHTYLEVY 712
Qy 664 IESEYEFTKTTVDKLIKTNLALVVGTHSMRDQMEALITVSAGADEDEDESGEERLPSCED 723
Db 713 IESEYEFTKTTVDKLIKTNLALVVGTHSMRDQMEALITVSAGADEDEDESGEERLPSCED 772
Qy 724 YVNHFLTVFMKVLFAVCPREYCHGACFRAVSLIIGMLTAITIGDLASHGCTIGLKDSY 783
Db 773 YVNHFLTVFMKVLFAVCPREYCHGACFRAVSLIIGMLTAITIGDLASHGCTIGLKDSY 832
Qy 784 TAVVFAFGTVPDTPFASKAALQDYADASIGNVTGSNANVNFELIGLAWSAALYMAL 843
Db 833 TAVVFAFGTVPDTPFASKAALQDYADASIGNVTGSNANVNFELIGLAWSAALYMAL 892
Qy 844 OQGEFVNSAGTLAFSVLTETFAVCISVLLYRRPHLGELGCGPRCKLATWLVSLW 903
Db 893 NGQOFVNSPPTLAFSVLTETFAVCISVLLYRRPHLGELGCGPRCKLATWLVSLW 952
Qy 904 LLYTLFATLEAYCYIKGF 921
Db 953 LLYTLFATLEAYCYIKGF 970

```

RESULT 2

S43730

Na+/Ca2+-exchanging protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Aug-2000

C:Accession: S43730

C:Furman, I.; Cook, O.; Kasir, J.; Rahamimoff, H.

FEBS Lett. 319, 105-109, 1993

A:Title: Cloning of two isoforms of the rat brain Na(+)-Ca(2+) exchanger gene and their

A:Reference number: S32435; MUID:93202244; PMID:8454039

Accession: S43730

Status: preliminary

Molecule type: mRNA

A:Residues: 1-935 <FUR>

A:Cross-references: EMBL:X68812; NID:g288229; PIDN:CAAA48707.1; PID:g288230

C:Superfamily: human Na+/Ca2+-exchanging protein

Query Match 71.7%; Score 3441; DB 2; Length 935;

Best local similarity 71.1%; Pred. No. 2, 2e-223;

Matches 673; Conservative 109; Mismatches 123; Indels 42; Gaps 11;

```

Qy 4 LRLQPLTSAFLHGLVTFVLF-----NGLRARAGSGDVPSTGQNNESGSGSDCK 55
Db 2 LRLSPNNSMGRFLVTLVLFTHVDHTADAEAGTGN-----ETTECTGSGYCK 53
Qy 56 EGVILPWPENSLDCKTARVIVFVALIYMFGLVSIADRMASLEVITSOEREYTK 115
Db 54 KGVILPWPENSLDCKTARVIVFVALIYMFGLVSIADRMASLEVITSOEREYTK 113
Qy 116 KPNGETSTTIRVWNETVSNLTALAGSSAPETLLSLIECHGIGTAGDGPSTIVGSA 175
Db 114 KPNGETSTTIRVWNETVSNLTALAGSSAPETLLSLIECHGIGTAGDGPSTIVGSA 173
Qy 176 ENKFTIIGICVYIPDGETRKIKHLRVFTTAAMSIFAYITWLTAVFSPGVVQWEG 235

```

RESULT 3

S32815

Na+/Ca2+-exchanging protein - human

N:Alternate names: Na+/Ca2+ antiporter; Na+/Ca2+ exchanger

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000

C:Accession: S32815; A56767

C:Komuro, I.; Wenninger, K.E.; Philipson, K.D.; Izumo, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 4769-4773, 1992

A:Title: Molecular cloning and characterization of the human cardiac Na(+)/Ca(2+) exc

A:Reference number: S32815; MUID:92262321; PMID:1374913

A:Accession: S32815

A>Status: preliminary

Molecule type: mRNA

A:Residues: 1-973 <IZU>

A:Cross-references: EMBL:M91368; NID:g180672; PIDN:AAA35702.1; PID:g180673

R.Kofuji, P.J. Hadley, R.W.; Kieval, R.S.; Lederer, W.J.; Schulze, D.H.

Am. J. Physiol. 263, C1241-C1249, 1992

A:Title: Expression of the Na-Ca exchanger in diverse tissues: a study using the clon

A:Reference number: A56767; MUID:93118744; PMID:1476165

A:Accession: A56767

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 4-253, 'K', 255-627, 'K', 629-692, 'K', 694-973 <KOP>
A:Note: sequence extracted from NCBI backbone (NCBI:121276, NCBI:121277)
C:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: cardiac muscle; heart; phosphoprotein; transmembrane protein

Query Match 71.7% Score 3439.5; DB 2; Length 973;
Best Local Similarity 68.9%; Pred. No. 2.9e-223;
Matches 674; Conservative 111; Mismatches 128; Indels 65; Gaps 10;

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QY 1 MAWLRLDPLTSAFLHFLVTVLFL-INGLRAEAGSGDVPSTGONNCSGSSDCKEGV 58
DB 4 MRRSLSPSTSMGHHLLVTVSLFSDHVAIETEMEGENETG-----CTGSYCKKGV 59
QY 59 ILPIWENPSLGDKIARVIVYFVALIYMLGVSIIADREMAIEVITSGREVTIKPN 118
DB 60 ILPIWEPQDSFGDKIRARVIVYFVALIYMLGVSIIADREMAIEVITSGREVTIKPN 119
QY 119 GEMSTTIRVWNETVSNLTLALGSSAPETLLSIEVCGHGFAGDGLGPTIVGSAFNM 178
DB 120 GETTKTVRIWNETVSNLTLALGSSAPETLLSIEVCGHGFAGDGLGPTIVGSAFNM 179
QY 179 FIIGICVUYIPDGETRKIKHLRVFTTAAMSIFAYIMLILAVFSFGVYQVMEGLTL 238
DB 180 FIIALCIVYVPOGETRKIKHLRVFTTAAMSIFAYIMLILAVFSFGVYQVMEGLTL 239
QY 239 FEPFVYVLAHVADKRLLFYKYMHHKYRTDKHNGIIEEGDHKRG---IEMDKMNSH 295
DB 240 FEPFICVAVMAVADRLLRYKYVKRYRAGKQGMIIIEHEDRPSSTEIEEMDKVNSH 299
QY 296 ---FLDGNLVLPBEKEVD---ESRREMIRILKOLKOKHPRKDDOLVEMANYALSIQ 348
DB 300 VENLIDALV-LEVDERDQDDEARREARILKELKOKHPRKELIOLLEIANVYL500 358
QY 349 KSRAFYRIQATRMKTGAGNLIKHAADQAKKASSMEVHTDEPE-DFISKVFPPCSYOC 407
DB 359 KSRAFYRIQATRMKTGAGNLIKHAADQAKKASSMEVHTDEPE-DFISKVFPPCSYOC 418
QY 408 LENCAGVLLTVVRKGDMSKTMVYDKTEDGSANAGADYEFTGTVLKPGETOKERSVG 467
DB 419 LENCAGVLLTVVRKGDMSKTMVYDKTEDGSANAGADYEFTGTVLKPGETOKERSVG 478
QY 468 IIDDIDIEEDENFVRLSNVRIEEOPEEGMPRAIENSILPRAYLASPCATATYIIDD 527
DB 479 IIDDIDIEEDENFVRLSNVRIEEOPEEGMPRAIENSILPRAYLASPCATATYIIDD 535
QY 528 HAGIETFECDTIHSESIGVMEVYVLRSGARGTVIVPRTVEGTAKGGEDFETGYEL 587
DB 536 HAGIETFECDTIHSESIGVMEVYVLRSGARGTVIVPRTVEGTAKGGEDFETGYEL 595
QY 588 EFKNDEVTYKTRIVDEEYERKQENFIALGEPKMMERG----- 627
DB 596 EFKNDEVTYKTRIVDEEYERKQENFIALGEPKMMERG----- 627
QY 628 -----ISDVTDRK--LIMEEERARIAEMGRPVVGEHPRKLEVI 663
DB 656 FGQPFVRKVAHREHILSTVITTIADYDDKPLTSKEEERRIAMGRPVVGEHPRKLEVI 715
QY 664 IEESYERKTVYDKLIKKTNLNLVVGTHSMRQDFMEALIVSAGDEDESEERLPSCFD 723
DB 716 IEESYERKTVYDKLIKKTNLNLVVGTHSMRQDFMEALIVSAGDEDESEERLPSCFD 775
QY 724 YVMHFLTVFVKVLFACVPRTYEGHGMACFAVSILIGMLTAIIGDLASHFECTIGLSDV 783
DB 776 YVMHFLTVFVKVLFACVPRTYEGHGMACFAVSILIGMLTAIIGDLASHFECTIGLSDV 835
QY 784 TAVAFVAFGTSVPTFPASKAALADYVADASIGVNTGSNANVFLGIGLASVAIYAL 843
DB 836 TAVAFVAFGTSVPTFPASKAALADYVADASIGVNTGSNANVFLGIGLASVAIYAL 895
QY 844 OGQEFHVSAGTLASVTLFTTFAFVCSVLLYRRRPHLGELGPRGCKLATTMLFVSLW 903
DB 844 OGQEFHVSAGTLASVTLFTTFAFVCSVLLYRRRPHLGELGPRGCKLATTMLFVSLW 903
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DB 896 NGEQFKVSPGTLAFSVTLFTTFAFVCSVLLYRRRPHLGELGPRGCKLATTMLFVSLW 955
QY 904 LLYLFATLFLAYCYIKRG 921
DB 956 LLYLFSSLEAYCHIKRG 973

RESULT 4

B53335
Na+/Ca2+-exchanging protein NCX1, splice form NACA6 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Aug-2000
C:Accession: B53335
R:Kofuji, P., Lederer, W.J., Schulze, D.H.
J. Biol. Chem. 269, 5145-5149, 1994
A:Title: Mutually exclusive and cassette exons underlie alternatively spliced isoform
A:Reference number: A53335; MUID:94148976; PMID:8106495
A:Accession: B53335
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-941 <KOP>
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBI:144050)
C:Superfamily: human Na+/Ca2+-exchanging protein

Query Match 71.7% Score 3437.5; DB 2; Length 941;
Best Local Similarity 71.0%; Pred. No. 3.8e-223;
Matches 669; Conservative 111; Mismatches 125; Indels 37; Gaps 11;

```
QY 8 PLTSAFLHFLGVTFLF-INGLRAEAGSGDVPSTGONNCSGSSDCKEGVLPWYPE 66
DB 9 PFSMGHLLALVALFFRVVDHVAETEMEGENETG-----CTGSYCKKGVLPWYRQ 64
QY 67 NPSLGDKIARVIVYFVALIYMLGVSIIADREMAIEVITSGREVTIKPNGETSTTI 126
DB 65 DPSEGDKIARVIVYFVALIYMLGVSIIADREMAIEVITSGREVTIKPNGETSTTI 123
QY 127 RVNNETVSNLTLALGSSAPETLLSIEVCGHGFAGDGLGPTIVGSAFNMFIIGICV 186
DB 124 RVNNETVSNLTLALGSSAPETLLSIEVCGHGFAGDGLGPTIVGSAFNMFIIGICV 183
QY 187 YVIRPGETRKIKHLRVFTTAAMSIFAYIMLILAVFSFGVYQVMEGLTLFEPFVYL 246
DB 184 YVIRPGETRKIKHLRVFTTAAMSIFAYIMLILAVFSFGVYQVMEGLTLFEPFVYL 243
QY 247 LAMVADKRLLFYKYMHHKYRTDKHNGIIEEGDHKRG---IEMDKMNSH---FLDGN 300
DB 244 LAMVADKRLLFYKYMHHKYRTDKHNGIIEEGDHKRG---IEMDKMNSH---FLDGN 303
QY 301 LVLPBEKEVD---ESRREMIRILKOLKOKHPRKDDOLVEMANYALSIQOQSAFARI 356
DB 304 LV-LVDYDERDQDDEARREARILKELKOKHPRKELIOLLEIANVYL500QSAFARI 362
QY 357 QATRMKTGAGNLIKHAADQAKKASSMEVHTDEPE-DFISKVFPPCSYOCLENCAGVL 415
DB 363 QATRMKTGAGNLIKHAADQAKKASSMEVHTDEPE-DFISKVFPPCSYOCLENCAGVL 422
QY 416 LTVVRKGDMSKTMVYDKTEDGSANAGADYEFTGTVLKPGETOKERSVGIIIDDIFE 475
DB 423 LTVVRKGDMSKTMVYDKTEDGSANAGADYEFTGTVLKPGETOKERSVGIIIDDIFE 482
QY 476 EDEHFFVLSNVRILEEOPPEEGMPRAIENSILPRAYLASPCATATYIIDDHAGITFE 535
DB 483 EDEHFFVLSNVRILEEOPPEEGMPRAIENSILPRAYLASPCATATYIIDDHAGITFE 539
QY 536 CDTHVSESIGVMEVYVLRSGARGTVIVPRTVEGTAKGGEDFETGYELGEKRNDETIV 595
DB 540 ESNVHVSISIMMEKVLRTSGARGTVIVPRTVEGTAKGGEDFETGYELGEKRNDETIV 599
QY 596 KTRIVKIVDEEYERKQENFIALGEPKMMERG-----ISDVTDRK--LIME 639
DB 600 KTRIVKIVDEEYERKQENFIALGEPKMMERG-----ISDVTDRK--LIME 659
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| | | | |
|----|-----|--|-----|
| Qy | 640 | EEBKARLAEKMPKPVLEGPKELEVIIEESYEFKTYVKKIKKLTALVGNHSDROEFMA | 699 |
| Db | 660 | EEERRRLAEKMPKPLGEHTKLEVIIEESYEFKSTYDKLIKLTALVYGTNSKREDFEIA | 719 |
| Qy | 700 | ITVSAAGDEDESGEERLSDSCFYVNHFLTFVFWKYLFAACVPPTXCHGAGFAVSILIT | 759 |
| Db | 720 | ITVSAGDEDDDDCEGEEKLSCSEFYVNHFLTFVFWKYLFAEVPPTXVWNGACFTVSIIMI | 779 |
| Qy | 760 | GLMFLAIIIGDLASHHGCGITIGLKDSTAVAVFAFGSPDPFASFAAALDOVYDASIGNT | 819 |
| Db | 780 | GLTLAFLIGDLASHHGCGITIGLKDSTAVAVFALGTSPDPFASFAAATDODYADASIGNT | 839 |
| Qy | 820 | GSNANVNFLLIGLGVAAAYMALOGGEHFVNSAGTLAFTVLTLEIAFVCISVLLYRRP | 879 |
| Db | 840 | GSNANVNFLLIGVAMSAIATYHANGGEHFVNSGTLAFTVLTLEIAFINVGLLYRRP | 899 |
| Qy | 880 | HLGGLGSPRGCRLATMFLPVSLLMLYLLPATLEAVCYINGF | 921 |
| Db | 900 | ETGGELGGPRAKTLTSCLEFLVLLATLTFSSLEACHINGF | 941 |

RESULT 5
2435

Na⁺/Ca²⁺-exchanging protein RBE-2 - rat
N:Alternate names: Na⁺/Ca²⁺ antiporter; sodium-calcium exchanger RBE-2
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Aug-2000
C:Accession: S32435
C:Furman, I.; Cook, O.; Kasir, J.; Rahamimoff, H.
FEBS Lett. 319, 105-109, 1993
A:Title: Cloning of two isoforms of the rat brain Na⁺(+)-Ca²⁺ exchanger gene and their
A:Reference numbers: S32435; MUID:93202244; PMID:8434039
A:Accession: S32435
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-958 <FUD>
A:Cross-references: EMBL:X60813; NID:q288231; PIDN:CA48708.1; PID:q288232
A:Superfamily: human Na⁺/Ca²⁺-exchanging protein

| | | | | |
|-----------------------|------------------|--------------------|-----------|------------|
| Query Match | 71.68 | Score 3434.5 | DB 2 | Length 958 |
| Best Local Similarity | 69.68 | Pred. No. 6.2e-223 | | |
| Matches 675 | Conservative 106 | Mismatches 124 | Indels 65 | Gaps 11 |

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0Y      4 LRLQJLTSFLEHFGVYTFPLFL-----NGLRAEAGSGDVPRSGQNNESGSSDDK 55
Db      2 LRLSLRPVNSMGRLLVTLVALLFTVHDHITADTEATGNN-----ETTECTSGSYCK 53
0Y      56 EGVILPIWPEMPSLGDKIARIVYFVALIYMFGLSVIADRFMASIEYTSQEREVTK 115
Db      54 KGVILPIHPEODPSGDKIARATYVFVAVNYVFLGSIIADRFMSIEYITSQERKITTK 113
0Y      116 KPNGETSTTIRVNNETVSNLTLMALGSSAPETLSLIEVCGHFIAGDLGPSTIVGSA 175
Db      114 KPNGETTKTIVRIHNETVSNLTLMALGSSAPETLSVIEVCGHNFAGDLGPSTIVGSA 173
0Y      176 FNMFIILIGCVYVIDGGERIKHLRVFFITAAWSFATIMLMLAVSPGVQVWEGE 235
Db      174 FNMFIILACVYVVDGGERIKHLRVFFVTAAWSFATIMWYIILSVSSPGVVEWEGE 233
0Y      236 LTFEFPACVLLAAVADRKLFLFYKMHKKYRFDKHNGIITLEDGHPK---TEMGSKM 292
Db      234 LTFEFPPLCVFAMVADRKLFLFYKRYRRAKQGMIIIEHGDGPASKTELEMGGKV 293
0Y      293 NSH---FLDGNLVPLEGKEVD---ESRREMTIRILKDLQKHPKEDLDLQVEMANYYS 345
Db      294 NSHVNFPLDGAIV-LEVERDODDDEAREMARILKELQKHPDKIEDLIELANQVUS 352
0Y      346 HQQSRARFYRIQATRMGTGAGNIIILKHAADQAKKASSMSEVHTDEPE-DFISKVFEPDPS 404
Db      353 QOQKSRARFYRIQATRMGTGAGNIIILKHAADQAKKAVSMHEVMDVYENDPVSKVFEEQGT 412
0Y      405 YQCLENCAGVLLTVVRKGGDMKTMVVDYKTEDGSNNAGADYEFTEGIVYVLRKGETQKE 464

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| | | | |
|----|-----|--|-----|
| Db | 413 | YQELNGCTVALTIIIRRGSGDLTNVDFDPTEDGTAGNASDYEFTEGTVLIPKGETQKRI | 472 |
| OY | 465 | SVGIIDDDIEFEDEHFFVRLSNRIIEEODPECGMPATFNSLPLPR-AVLASECAVATVI | 523 |
| Db | 473 | RVGIIDDDIEFEDEHFNFLVHLSNVASVESEDDG-----ILDSNHVSAIACISGPNATITRI | 528 |
| OY | 524 | LDDHAGIEFTEECOTIHVSISIGIMEVKVLRITSGAGTGVPRPRTVETGAKGGGEDEDT | 583 |
| Db | 529 | PDDHAGIEFTEEPVTVSESIGIMEVKVLRITSGARGNVLIIPKTIETGARGGGEDEDT | 588 |
| OY | 584 | YGELIEKADETVKTIIRVKIYDEEEREQENFIALGPKMER----- | 626 |
| Db | 589 | CGELEFOENDELVKTIISKVVIDDEYEKKNFFLEIGSRPLVEMSEKKGFRTLQGVYERK | 648 |
| OY | 627 | -----GISVDTRK--LIMEEENAKRIAMKPVUGIEHPKLEVIIEESYEK | 671 |
| Db | 649 | VHARDPIPTSVIISSEYEDKOPLTSEEEERRIAMGPRILIEHTKLEVIIEESYEK | 708 |
| OY | 672 | TTYVKLTKKTLALVYGTSHSMRODFMAITVISAAGDEDEDESEERLPRSCFYVHMFLLV | 731 |
| Db | 709 | STVCLKIKKTLALVYGTNSRQDFLEAITVISAAGEDDDDECEERLPRSCFYVHMFLLV | 768 |
| OY | 732 | FMKVLFACVPTREYCHGMACEFAVSIILIGMLTPIIGDLSHFECTIGLDSYAVVFAV | 791 |
| Db | 769 | FMKVLFAFVPTREYVWGNACFIYSIIMTIGLTLAFIGDLSHFECTIGLDSYAVVFAV | 828 |
| OY | 792 | GTSVPDEFASKAALADQVYADASIGNVTGSANVNF.LGIGLASVNAIYMALOGQEFHVS | 851 |
| Db | 829 | GTSVPDEFASKAVATDQYADASIGNVTGSANVNF.LGIGLASVNAIYHANAGDEQKVS | 888 |
| OY | 852 | AGTLAFSVTLFTTITAFVCIISVLLYRRRPHLIGELGCRCKLATIYVLSMLYILENT | 911 |
| Db | 889 | PGLTAFSVTLFTTITAFINVGVLVYRRRPEITGELGCRPKLKTLSLPVLLMLLYIFESS | 948 |
| OY | 912 | LEAYCYIKGF | 921 |
| Db | 949 | LEAYCHINGF | 958 |

RESULT 6

I48097
 Na+/Ca2+-exchanging protein - guinea pig
 C:Species: *Cavia porcellus* (guinea pig)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Aug-2000
 C:Accession: I48097
 R:Tsutsurya, Y.; Bersohn, M.M.; Li, Z.; Nicoll, D.A.; Philipson, K.D.
 Blochm. Biophys. Acta 1196, 97-99, 1994
 A:Title: Molecular cloning and functional expression of the guinea pig cardiac Na(+)-
 A:Reference number: I48097; MUID:95078257; PMID:7986817
 A:Accession: I48097
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-970 <RES>
 A:Cross-references: EMBL:U04955; NID:9927230; PIDD:AAA73904.1; PID:9507350
 C:Superfamily: human Na+/Ca2+-exchanging protein

| | | | | |
|-----------------------|-------------------|---------------------|------------|-------------|
| Query Match | 71.6%; | Score 3432.5; | DB 2; | Length 970; |
| Best Local Similarity | 68.7%; | Pred. No. 8.5e-223; | | |
| Matches 672; | Conservative 112; | Mismatches 129; | Indels 65; | Gaps 11; |

[illegible]

[illegible]

Db 416 LENTVALTLIIRRGDGLINTVFVDFTEDGTANAGSDYFECTGVFKRGKQKEIRVG 475

Qy 468 IIDDIDFEEDHEFFVRLSNVRIEEOPECHPPLIINSLPLPRAVLASPCVAATYTIIDD 527

Db 476 IIDDIDFEEDHEFFVRLSNVRIEEOPECHPPLIINSLPLPRAVLASPCVAATYTIIDD 532

Qy 528 HAGITFEPCDTHIHSESIIGVMEVVLRTSGARGVIVPFRTEGTAKGGDEDFDTGEL 587

Db 533 HAGITFEPCDTHIHSESIIGVMEVVLRTSGARGVIVPFRTEGTAKGGDEDFDTGEL 592

Qy 588 EFKNDYFKTRVKKIVDEEEXEROENFIALGEPKRMERG----- 627

Db 593 EFKNDYFKTRVKKIVDEEEXEROENFIALGEPKRMERG----- 652

Qy 628 -----ISDVTDRK--LMEEBEAKRIAEKMKPVUGENPKLEVI 663

Db 653 YGQPVFRKHAREHPLPSTIITITIDEYDDKQPLTSKEEERKRIAEKMKPVUGENPKLEVI 712

Qy 664 IEESEFFETVADKLIKKNLALVGTSHMRQFMEATITVSAAGDEDESGEERTLPSCFD 723

Db 713 IEESEFFETVADKLIKKNLALVGTSHMRQFMEATITVSAAGDEDESGEERTLPSCFD 772

Qy 724 YMHPLTFYFWKVLFAFVDPTEYCHGMACFAVSIILIGMLTAITGLDSHFGCTIGLDSV 783

Db 773 YMHPLTFYFWKVLFAFVDPTEYCHGMACFAVSIILIGMLTAITGLDSHFGCTIGLDSV 832

Qy 784 TAVVFAVAGTSVPDTFASKAALODVADASIGVATSGNNAVNFVLGIGLMSVAATYIWA 843

Db 833 TAVVFAVAGTSVPDTFASKAALODVADASIGVATSGNNAVNFVLGIGLMSVAATYIWA 892

Qy 844 OGOEHFVAGTFLAFSVLTFTIFAFVCIISVLLYRRRPHIGELGSPRCCKLATYMLFVSLW 903

Db 893 NGEQKVPSPGLAFSVLTFTIFAFVCIISVLLYRRRPHIGELGSPRCCKLATYMLFVSLW 952

Qy 904 LLYIFATLEAVCYIKGF 921

Db 953 LLYIFATLEAVCYIKGF 970

RESULT 9

S28833

Na+/Ca2+-exchanging protein - rat

N:Alternate names: Na+/Ca2+ antiporter; Na+/Ca2+ exchanger

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000

C:Accession: S28833; S25552

R:Low, W.; Kasir, J.; Boulter, J.; Heilmann, S.; Rahamimoff, H.

FEBS Lett. 316, 63-67, 1993

A:Title: Cloning of the rat heart Na(+)-Ca(2+) exchanger and its functional expression

A:Reference number: S28833; MUID:93138118; PMID:8422940

A:Accession: S28833

A:Molecule type: mRNA

A:Residues: 1-971 <LOW>

A:Cross-references: EMBL:X68191; NID:957208; PIDN:CAA48273.1; PID:957209

R:Low, W.; Kasir, J.; Boulter, J.; Heilmann, S.; Rahamimoff, H.

submitted to the EMBL Data Library, August 1992

A:Reference number: S25552

A:Accession: S25552

A:Molecule type: mRNA

A:Residues: 1-194, 'F', 196-971 <LO2>

A:Cross-references: EMBL:X68191

C:Superfamily: human Na+/Ca2+-exchanging protein

C:Keywords: ion transport; membrane protein; phosphoprotein

Query Match 71.3%; Score 3422; DB 2; Length 971;

Best Local Similarity 68.6%; Pred. No. 4, 4e-22;

Matches 674; Conservative 106; Mismatches 125; Indels 78; Gaps 11;

4 LRLQPLTSAFLHFGIVTFVFL-----NGLRAEAGSGDVPSTGQNNESGSGSDCK 55

||||| : : ||||| | ||||| : ||||| |

2 LRLSLPRAVNSGFRVLTVALLPFHVDHTADTAEAFNGN-----ETTECGSGSYCK 53

56 EGVILPLWIPENPSLGDKIARVIVFVALIYMEIGVSIINDRPNASIEVITTSQREYVTK 115

Db 54 KGVILPIHEPQDPSFGDKIARATVYFVAWVYMLGVSIIADRFMSSEIVTSQEKETIK 113
Oy 116 KPNGETSTTTIVNMEYTSNLTLMALGASAPILLSLIEVCHGFLAGDLPSTIVGSA 175
Db 114 KPNGETSTTTIVNMEYTSNLTLMALGASAPILLSLIEVCHGFLAGDLPSTIVGSA 173
Oy 176 FMFPIIGICVVIDGGERIKHLRVFPIITAMSSIFATIMLYMLTAVSPGVOWEGL 235
Db 174 FMFPIIALCVTVVPDGETRIKHLRVFPIITAMSSIFATIMLYMLTAVSPGVOWEGL 233
Oy 236 LTFEFPVOLLAWYADKRLFLYKYMHKYRTDKHGIIEETEGDHPKQ---IENDGKMA 292
Db 234 LTFEFPVOLLAWYADKRLFLYKYMHKYRTDKHGIIEETEGDHPKQ---IENDGKMA 293
Oy 293 NSH---FLDGNLVLEGEKV---ESRREMRILKDLKQKPERDLOLVEMANYALS 345
Db 294 NSHVNFLDGNLV---LEVERDODDEARERARILKELQKHPRKEIEQLIELANYQVLS 352
Oy 346 HQKRAFRIOATMMTGAGNLLKKAHAAEQAKKASMEVHTDEPE--DFISKVPFDPQS 404
Db 333 HQKRAFRIOATMMTGAGNLLKKAHAAEQAKKASMEVHTDEPE--DFISKVPFDPQS 412
Oy 405 YOCLENCGAVLLTVYRKGGDSKTMVVDYKTEDGSANAGADETEGTVVLPKGETOKEF 464
Db 413 YOCLENCGAVLLTVYRKGGDSKTMVVDYKTEDGSANAGADETEGTVVLPKGETOKEF 472
Oy 465 SVGIIDDDIFEEDEHFYRLSVRIEEOPEGMRAPEINSLPLPR--AVLASPCVATVTI 523
Db 473 RGIIDDDIFEEDEHFYRLSVRIEEOPEGMRAPEINSLPLPR--AVLASPCVATVTI 528
Oy 524 LDDHAGITFECDTIHVESIGVMEVKVLRSGARTVYFPRVREGAKSGEDFEDT 583
Db 529 FDDHAGITFECDTIHVESIGVMEVKVLRSGARTVYFPRVREGAKSGEDFEDT 588
Oy 584 YGELEFKNDEYKTIKVIKIVDEEYERODNFIALGEPKMER----- 626
Db 589 GCELEFONDEIKTISVKYIDDEYEKNTFEIIEGEPFLVEMSEKALLNDELGFTLT 648
Oy 627 -----GISVDYDRK--LTMEEDAKRIEMKGPVUGHP 658
Db 649 ECKKMYGQVPRKVARHARPIRSTVYISISEYDDKQPLSKSEERIRIEMKRPILGEHT 708
Oy 659 KLEVIIESEYKFTVVDKLIKTNLALVYTHSMRDQFMEATVYSAAGDEDESEGEHT 718
Db 709 KLEVIIESEYKFTVVDKLIKTNLALVYTHSMRDQFMEATVYSAAGDEDESEGEHT 768
Oy 719 PSCFDYVMHFLTVFMKVLFAFVPRPEYMGMACFIVSILMIGLTLAFIGDLASHGECTIG 828
Db 769 PSCFDYVMHFLTVFMKVLFAFVPRPEYMGMACFIVSILMIGLTLAFIGDLASHGECTIG 828
Oy 779 LKDSYTAAYFAVFGTSVPDTPFASKAALADYVADASIGNVTSNNAVNFGLGILAWSVA 838
Db 839 LKDSYTAAYFAVFGTSVPDTPFASKAALADYVADASIGNVTSNNAVNFGLGILAWSVA 888
Oy 839 IYMALOGEYHAGTAFSVTLTFIFAVCSVLLYRRRPHLGGELGPRCKLATYTL 898
Db 889 IYMALOGEYHAGTAFSVTLTFIFAVCSVLLYRRRPHLGGELGPRCKLATYTL 948
Oy 899 FVSLMLYLTFATLEAYCYIKGF 921
Db 949 FVSLMLYLTFATLEAYCYIKGF 971

RESULT 10
A:Accession: A54139
Na+/Ca2+-exchanging protein NCX2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 18-Aug-2000
C:Accession: A54139
R:Li, Z.; Matsuda, S.; Hryshko, L.V.; Nicoli, D.A.; Bersohn, M.M.; Burke, E.P.; Lifton, J. Biol. Chem. 269, 17434-17439, 1994
A:Title: Cloning of the NCX2 isoform of the plasma membrane Na(+)-Ca(2+) exchanger.

A:Reference number: A54139; MUID:94292496; PMID:8021246
A:Accession: A54139
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-921 <L1>
A:Cross-references: GB:008141; MID:9511680; PIDN:AAA19920.1; PID:9511681
C:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: transmembrane protein

Query Match 70.0%; Score 3357; DB 2; Length 921;
Best Local Similarity 69.6%; Pred. No. 9, 6e-218;
Matches 635; Conservative 130; Mismatches 114; Indels 34; Gaps 9;

Oy 31 EAGSGSDVPSIQONNE-----SCSGSDCKEYVILPIWPEPNSGDKIARIVYVVALI 85
Db 21 EATPPSPPLPPANDSDASPGGQSGYRCQPGVLLVWPEBDDPSLDKAAARVYVVAAY 80
Oy 86 YMFGLGSIADRFMASIEYTSQEREVTIKKPNGETSTTIRVNMETVSNLTLMALGSSA 145
Db 81 YMFGLGSIADRFMASIEYTSQEREVTIKKPNGETSTTIRVNMETVSNLTLMALGSSA 140
Oy 146 PETLLSLIEVCGHGFAGDLPSTIVGSAAFNMFIIGICVYVIPDGETRIKHLRVFPI 205
Db 141 PETLLSLIEVCGHGFAGDLPSTIVGSAAFNMFIIGICVYVIPDGETRIKHLRVFPI 200
Oy 206 TAAVSFAITIMLYMLTAVSPGVOWEGLLTFEFPVOLLAWYADKRLFLYKYMHKY 265
Db 201 TAAVSFAITIMLYMLTAVSPGVOWEGLLTFEFPVOLLAWYADKRLFLYKYMHKY 260
Oy 266 PRDKHGIIEEGDHPKGIEMDKMMNSHFLDGNL---VPLEGKEVDESREMRILY 320
Db 261 PRDKHGIIEEGDHPKGIEMDKMMNSHFLDGNL---VPLEGKEVDESREMRILY 319
Oy 321 KDLQKHPRKDLQVLEMANVYALSHQKSRAPYRIQATMMTGAGNILLKKAHAAEQAKA 380
Db 320 KDLQKHPRKDLQVLEMANVYALSHQKSRAPYRIQATMMTGAGNILLKKAHAAEQAKA 379
Oy 381 SSMSEVHTDEPDEFTSKVFEFDCPSVOCLENCGAVLLTVYRKGGDSKTMVVDYKTEDGSA 440
Db 380 GA--NDGAPDEDDGASRIPEPSLYHCLNCGSVLLSVACQGGEGNSTYVYDTRFEDGSA 438
Oy 441 NAGADETEGTVVLPKGETOKEFVGIIDDDIFEEDEHFYRLSVRIEEOPE---PEE 496
Db 439 NAGADETEGTVVLPKGETOKEFVGIIDDDIFEEDEHFYRLSVRIEEOPE---PEE 498
Oy 497 GMPRAIENSLPLPRAYLAPCVATVTIIDDHAGITFECDTIHVESIGVMEVKVLRYS 556
Db 499 G-----GRPKGRVLAPLATVTLIDDHAGITFECDTIHVESIGVMEVKVLRYS 549
Oy 557 GARTVYFPRVREGAKSGEDFEDTGELEKNDYKTIKVIKIVDEEYERODNFIALGEPKMER 616
Db 550 GARTVYFPRVREGAKSGEDFEDTGELEKNDYKTIKVIKIVDEEYERODNFIALGEPKMER 609
Oy 617 ALGEPKMERGISTDYV-----DRKLTMEEDAKRIEMKGPVUGHPKLEVIIESEYF 670
Db 610 ALGEPKMERGISTDYV-----DRKLTMEEDAKRIEMKGPVUGHPKLEVIIESEYF 669
Oy 670 ELGQFQMLKRGISALLNNGDDRKTLAEEERQRIAEKGRYVLGNCLELYIEESYDF 728
Db 729 ELGQFQMLKRGISALLNNGDDRKTLAEEERQRIAEKGRYVLGNCLELYIEESYDF 728
Oy 729 LTFEFPVOLLAWYADKRLFLYKYMHKYRTDKHGIIEETEGDHPKQ---IENDGKMA 788
Db 729 LTFEFPVOLLAWYADKRLFLYKYMHKYRTDKHGIIEETEGDHPKQ---IENDGKMA 788
Oy 789 VAFGTSVPDTPFASKAALADYVADASIGNVTSNNAVNFGLGILAWSVAIYMALOGEY 848
Db 789 VAFGTSVPDTPFASKAALADYVADASIGNVTSNNAVNFGLGILAWSVAIYMALOGEY 848
Oy 849 HVSAGTIAFSVTLTFIFAVCSVLLYRRRPHLGGELGPRCKLATYTLFVSLMLYL 908
Db 849 HVSAGTIAFSVTLTFIFAVCSVLLYRRRPHLGGELGPRCKLATYTLFVSLMLYL 908

OY 909 FATLEAYCYIKGF 921
DB 909 FASTLEAYCHIRGF 921

RESULT 11

B89047

protein C1068.5 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

C:Accession: B89047

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; PMID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C_eleg

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: B89047

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-890 <STO>

A:Cross-references: GB:chr_V; PIDN:AAB09172.1; PID:g1572830; GSPDB:GN00023; CESP:C1068.5

Genetics:

A:Gene: C1068.5

A:Map position: 5

C:Superfamily: human Na⁺/Ca²⁺-exchanging protein

Query Match 41.8%; Score 2007; DB 2; Length 890;

Best Local Similarity 45.9%; Pred. No. 6.8e-127;

Matches 416; Conservative 145; Mismatches 232; Indels 114; Gaps 13;

OY 87 MFLGVSIADRFMASIEVITSOEREVYIKRPNGETSTTIRVWNETVSNLTMLAGSSAP 146

DB 1 MFLGISIVADRFMSIEVITSMERTIVYKRPGLDPMAYVRIMNDIVSNLTMLAGSSAP 60

OY 147 ELLLSIEVCGHGFIADGLPSTIVGSAFNMFTITICIVYVDPDGTTRIKHLRVFTT 206

DB 61 ELLLSIEVARGFEADGLPNTIVGSAFNLPMIADICVIVIPKGIROKHLDFVCVT 120

OY 207 AANSIFAYILVYMLTAVFSGVQVWEGLLTLPFFPVCLLAWADKRLLEFYKMHKKYR 266

DB 121 ATMSVYFVWLYLILAFSGEIEIMGALTFEPLTVTAIYADIKLONKFLPHRYR 180

OY 267 TDKRGLIIEEDGHPKGIEMDKMNSHFLDGLVPLEGKEVDESRREMIIRILKDKQ 326

DB 181 RGSN-GQMINTAEEMKMLE-----NGTQGPALKAFEEHNGEITELMREIRKQ 228

OY 327 HPEKDLQVEMANYIALSHQOKSRAFYRIQATRMATGACNILLKHAEDAKKA-SSMSE 385

DB 229 NPHTPELQKQAEYEMISGRPKSRAFYRVQATRRILIGCDIYKRIKIDKHNKALDALVQ 288

OY 386 VHRDEPDEFTSKYFEDPCSYQCLENGAVLLTVVRKGGDKMTYVYKTEDGSANAGAD 445

DB 289 AOEQSDNCKTFLDPAHNTVLESFVYVGRDGGPGLTVMDVFTEDGSANAGSD 348

OY 446 YEFTEGTIVLKPGETOKESFVGIIIDDFEEDHEFVRLSNVRIEBOPEG--MPPAIF 503

DB 349 YIPKGTGLTFYEDKHKQVITEVDDVFEDEHFLYRLCNLRY--RTKDGIIIDPTRI 405

OY 504 NSLPLPAVLAAPCAVATVTLDDDHAGITFEEDCTIVSSIGVMEKXVLTSGARSTVI 563

DB 406 GGLPVA--AQLEMPATATIMLDDHAGVFGFEHDHFQVENCGLSLQMKRHSGARKEVI 463

OY 564 VPPEFTVGTAKGGDEDEDYGELEFKNDETVKTIKVIYDEDEYEHOENFTALGSPK 623

DB 464 IIPRTVGTGA-SADKHEEMKEGELVEFEDNOTALVEIGIYDTEQYKSDYFTIELSPW 522

OY 624 -----MERGISDVTDRK-----LTMBEEA 643

DB 523 AKKMDLSRIQERFORMERKRGSSVASSEKSDSTENALAPAEKSTRAASVDLQPSDP 582

OY 644 KR-----IAEMGKPVILGEHPKL 660

DB 583 RRSQNTSPHLTSFRNRRLGSMIAGMKGNGBDEVTTSLTPSOLEIAEMGKPRILGEFTKC 642

OY 661 EVLIEESEYEFKTTVDKLIKRTNLTALVYGTSHMRDQMEATVTSAGDEDED---ESGEE 716

DB 643 QITRESKEFGIVDRKIKANANRIMGTHSMWQEFREALVYASGDDDDDEGEDGE 702

OY 717 R---LPSCFDYVNHFLTVEMKVLFCACVPPTREYCHGMACEPAVSILIIIGMTAIGDLASHF 773

DB 703 KEPEEPGCMXYMNHVLTVPKRLTFATIPRDPYFGMATFVAALFMIGVLTAAVAGDLASQF 762

OY 774 GCTIGLKDSTAYVFAVFGSVDPDTFASKAAALQDYADASIGNYGSNANVNFILGILA 833

DB 763 GCGWGLKDAYTAISFVALGTSVDPDTFASKVSAVQDKTADNAVGNVGSNANVNFILGILA 822

OY 834 MSVAATYMALOGGEFHVSAAGTIAFSVTLFTFPAFCISVLYRRRPHLKGELGSPRCXL 893

DB 823 WSNAAITYHMOGKRLVLPDPNIGFSVILFCTEAVLCITIVLARKNKVGGELGPIALRL 882

OY 894 ATTWLFV 900

DB 883 T---IFV 886

RESULT 12

T24110

hypothetical protein ZC168.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T24110; T27507

R:Berts, M.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19841

A:Accession: T24110

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-807 <WILL>

A:Cross-references: EMBL:Z70309; PIDN:CAA94363.1; GSPDB:GN00022; CESP:ZC168.1

A:Experimental source: clone R102

R:Berts, M.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z20378

A:Accession: T27507

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-807 <W12>

A:Cross-references: EMBL:Z70312; PIDN:CAA94387.1; GSPDB:GN00022; CESP:ZC168.1

A:Experimental source: clone ZC168

C:Genetics:

A:Gene: ZC168.1

A:Map position: 4

A:introns: 38/1; 177/3; 346/1; 365/1; 369/3; 414/3; 455/3; 692/3; 743/2

Query Match 24.8%; Score 1192; DB 2; Length 807;

Best Local Similarity 33.6%; Pred. No. 4.3e-72;

Matches 302; Conservative 150; Mismatches 320; Indels 126; Gaps 20;

OY 47 SCGSSSDCKEGLVPIYPENPSLGDKIARIYVYFVALIMFGVSIADRFMASIEVIT 106

DB 2 SSSANLCKNGKIGLL-----PALETPRNAIILYAGLFCFGLIAADIPMSIEQIT 54

OY 107 SQREYVYIKRPNGETSTT-----IRVWNETVSNLTMLAGSSAPETLLSILEY 155

DB 55 SATKRYKKQKAKOLVAKEDEIDEQYDVYRIMNPVANTLMAAGSSAPELISIEI 114

OY 156 CGHGTIAGDGPSTIVGSAFNMFTITICIVYVDPDGTTRIKHLRVFTTAMSTFAYI 215

DB 115 VGNQFAGDGPSTIVGSAFNLFCISALCEVAV-GTQRIKRIELRYEVVTAFFGTPAYI 173

OY 216 WLYMILAVFSGVQVWEGLLTLPFFPVCLLAWVADKRLLEFYKMHKKYRTD----- 268

DB 174 WFLVLYVITPNVYDVAELITLIFLLVYVSYADAQI-----WKKKSSDLOELEM 228

OY 269 -KHGIIIEEDGHPKGIEMDKMNSHFL-----DGNLVPLEGKEVDESRREMIIRILKDL 323


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Db 229 AOHGKV-----DDQPEKLSDEIKKMASNLSLNKEENDVIADTPSVDTVR-----KMTSRI 280
Qy 324 KOKHPEKLDLVEMANYALSHOOKSRAFYRIQATRMGTAGNLKKAHDAQKAKASM 383
Db 281 SHYTPSLSEDOAKITLAVRSRTNSHRLYYRIRAIRQLSSS--WRKSEEEVLMKMNQ 337
Qy 384 SEVHTDEPEDFISKVEFPDPCSYOCLENGCAVLLFVRKGGMSKMTWYDYTETDGSANAG 443
Db 338 ES--TDSASRRKTYEFEFARARYRDATDETYSLEKTERK-GNNESEFTYSYATVNLAKD 394
Qy 444 ADYEETECTVVLKRGETOKESVGIIDDDIFEEDHEFVRLSNVRIEEOEGEMPATF 503
Db 395 LNFLEKSTLOPNFGEHLKTIISQILNANMRPNDFVHLKIQOVDD-----443
Qy 504 NSLPLRAVLASPCVAVTYTIIDDHAGIFTEECDTIH-VSESIGVMEKVLRTSG-ARGT 561
Db 444 -----SKICIGA-----CNVAHVYKKNAGFSRSFVTRRGKLLKP 478
Qy 562 VVPRFVEGTAKGGDEDFEDTYGELFEKNDETVTKIVDEEYERQENFTALGEP 621
Db 479 LQVHETEDVAKOGDDTTAVKDGILGEGEYKEYIDIVIDMKDEAFIIEI-L 536
Qy 622 KMERGISDVTDRKLTMEEBEAKRIAEMGKPVLGEPHLEVIIESEYEFK--TYVDKLIK 679
Db 537 KVDEGVSIGTRRKATI-----TIISDNVKNITNTRKLMG 573
Qy 680 KTNLALVGVTHSMRDQMEAITVSAAGDEDESGEERLPSCFDYVHMFVEMKVLPAK 739
Db 574 HYMRLOIRGKATWKEOILNAVSVNA-----GDLNANVYSDCILHALFPMFAFAE 624
Qy 740 VPPEYCGMACFANVSIILGLMTAIIIGDLASHFGCTIGLSDVTAVVFAVFGTSVPPTF 799
Db 635 LPPPIIFGTCFVVALIGIVTAVGVDSIFECMGGLDAMVATRLVALGSLPDTF 684
Qy 800 ASKAAALODVYADASIGNVTSNANVFLGIGLANSVAIYALOGEFHVSAGTLAFSV 859
Db 685 ASKIAESDPTADNANVGVTSNSVNFVLGILPVIASLVWASGSEFRVADAGLGFSV 744
Qy 860 TLFITFAVCTISVLLYRRRPHL--GGEIGCRGCKLATTWLVSLMLYLIFATIEAY 915
Db 745 TVFMICSVLFLVVLVLRKRLKAFGOGELGPGFTKLSALFEFVGLMIYVGLSIKMY 802

RESULT 13
A:Species: Rattus sp. (rat)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 18-Aug-2000
C:Accession: 152640
R:Morlier, L.N.; Zheng, T.; Tang, J.; Grayson, D.R.
Brain Res. Mol. Brain Res. 20, 21-39, 1993
A:Title: Regional distribution in the rat central nervous system of a mRNA encoding a p
A:Reference number: 152640; MUID:94077033; PMID:8255180
A:Accession: 152640
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-152 <RES>
A:Cross-references: GB:S67769; NID:9459304
C:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: cardiac muscle; heart

Query Match 13.7%; Score 659; DB 2; Length 152;
Best Local Similarity 82.9%; Pred. No. 3e-37;
Matches 126; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
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Qy 820 GSNANVFLGIGLANSVAIYALOGEFHVS 851
Db 121 GSNANVFLGIGLANSVAIYALOGEFHVS 152

RESULT 14
A:Alternative names: hypothetical protein T30822.10
N:Alternate names: hypothetical protein T30822.10
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C:Accession: T00424; C84917
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; M
submitted to the EMBL Data Library, October 1998
A:Description: Arabidopsis thaliana chromosome II BAC T30822 genomic sequence.
A:Reference number: 21419
A:Accession: T00424
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-538 <ROU>
A:Cross-references: EMBL:AC002535; NID:92529657; PID:93522931
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84917
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <STO>
A:Cross-references: GB:AE002093; NID:93522931; PID:NAC62871.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g47600; T30B22.10
A:Map position: 2
A:Introns: 131/1; 189/3; 229/2; 287/1; 333/1; 397/1; 440/2

Query Match 12.0%; Score 573.5; DB 2; Length 538;
Best Local Similarity 22.2%; Pred. No. 1e-30;
Matches 191; Conservative 107; Mismatches 195; Indels 369; Gaps 22;
```

| | | | | |
|----|-----|--|--|----------------------|
| Db | 276 | ----- | IF----- | SI 279 |
| Qy | 540 | HVSESIGMEVKULTRSGARCTVYVPRRYBGTAKGGEDFEDTGYELFKNDYKTR | | 599 |
| Db | 280 | H----- | SANDNGITHTYAADTPP----- | DSATKKG 306 |
| Qy | 600 | VKIVDEEYERQENFIALGEPKMMERGISDVTDRKLTMEEEKARIAEMGRPVLGBHPK | | 659 |
| Db | 307 | AK----- | | 308 |
| Qy | 660 | LEVIIESEYEKTTVDKLIKKTALNALVGHSHWDOFMEAITVSAGADEDEDESGEERLP | | 719 |
| Db | 309 | ----- | NSHVFDI----- | WKHOEVDIAITVKIF----- |
| Qy | 720 | SCDFYV----- | MFLVYEMKVLFEACYPPTREYCHGACAFVSLILITGMLTAITIGDLASHF | 773 |
| Db | 333 | MDSTYLRIAKSEFWHLLAPMKLLFEAPPCNIAHGMATFICSLFTISGAFAVYTRFTDIL | | 392 |
| Qy | 774 | GCTTGLKDSYAAVVAEFGTSVPPTFASPKAAALODVADASIGNVNGSNVNFYLGIA | | 833 |
| Db | 393 | SCVGININRYVIAFALASGTSMPULVASKRTAERQULTADSAINITCSNVNITGVIGVP | | 452 |
| Qy | 834 | WSVAAI--YMALQOEHFVSAAGTLAFSVLTFTFAFVCISVLVYRRRPHLGGELGPRGC | | 891 |
| Db | 453 | WLINTVYVYFAFYREPLYENNAKGSFLILFEFATSVGCIWLVLRRL--IIGAEGLGPRLM | | 511 |
| Qy | 892 | KLATWTLFVSLMLXLYIFATLE | | 913 |
| Db | 512 | AMLTSAFEMKLMVVEFVLSLAK | | 533 |

RESULT 15

Na+/Ca2+-exchanging protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 18-Aug-2000
C:Accession: A48852
R:Yu, A.S.; Hebert, S.C.; Lee, S.L.; Brenner, B.M.; Lytton, J.
Am. J. Physiol. 263, F680-F685, 1992
A:Title: Identification and localization of renal Na(+)-Ca2+ exchanger by polymerase chain reaction
A:Reference number: A48852; MUID:93035974; PMID:1415740
A:Accession: A48852
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-133 <YU1>
A:Experimental source: kidney
A:Note: sequence extracted from NCBI backbone (NCBI:P.116872)
C:Superfamily: human Na+/Ca2+-exchanging protein

| | | | | |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match | 11.9%; | Score 573; | DB 2; | Length 133; |
| Best Local Similarity | 84.2%; | Pred. NO. 1.5e-31; | | |
| Matches 112; Conservative | 7; | Mismatches 14; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---|-----|
| 0Y | 730 | TFNKKVLEFACBPPEYECGNACFAVSLITIGMLTAITGDLASHGGCTIGKDSVTAAVEV | 789 |
| | | 1 TFNKKVLEFANVPPEYINMGWACFTVSLITIGMLTAITGDLASHGGCTIGKDSVTAAVEV | 60 |
| 0Y | 790 | AFGTSVPDTEFASKAALODVYVADASIGNVTGSMNAVNEFLIGLAMSVAALYMALOGOEPH | 849 |
| | | 1 ALGTSVPDTEFASKAALODVYVADASIGNVTGSMNAVNEFLIGLAMSVAALYMALOGOEPH | 120 |
| 0Y | 850 | VSAGTLAFSVTLF | 862 |
| | | 1 VSAGTLAFSVTLF | 133 |

Search completed: November 30, 2002, 12:32:08
Job time : 35.6762 secs